

SEQUENCE LISTING

<110> NsGene
Biogen, Inc.
Johansen, Teit E.
Sah, Dinah Wen-Yee

<120> Novel Neurotrophic Factors

<130> 00689-511 PCT (C045 CIP) NBN

<140> Filed Herewith

<141> 2002-02-28

<150> DANISH 1998 00904

<151> 1998-07-06

<150> USSN 60/092,229

<151> 1998-07-09

<150> DANISH 1998 01048

<151> 1998-08-19

<150> USSN 60/097,774

<151> 1998-08-25

<150> USSN 60/103,908

<151> 1998-10-13

<150> DANISH 1998 01265

<151> 1998-10-06

<150> U.S.S.N 09/347,613

<151> 1999-07-02

<150> U.S.S.N 09/804,615

<151> 2001-03-12

<160> 57

<170> PatentIn Ver. 2.1

<210> 1

<211> 865

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (120)..(719)

<220>

<221> 5'UTR

<222> (1)..(119)

<220>

<221> 3'UTR

<222> (721)..(865)

<220>

<221> sig_peptide

<222> (120)..(179)

<220>

```

<221> mat_peptide
<222> (405)..(719)

<220>
<221> misc_structure
<222> (661)..(663)
<223> CARBOHYD: Glycosylated Asparagine at Asn87

<220>
<221> misc_structure
<222> (426)..(623)
<223> DISULFID - Cys8-Cys73 disulfide bridge

<220>
<221> misc_structure
<222> (507)..(707)
<223> DISULFID: Cys35-Cys101 disulfide bridge

<220>
<221> misc_structure
<222> (519)..(713)
<223> DISULFID: Cys39-Cys103 disulfide bridge

<220>
<221> misc_structure
<222> (616)..(619)
<223> DISULFID: Cys72-Cys72 interchain disulfide bridge

<400> 1
ctaggagccc atgcccggcc tgatctcagc ccgaggacag cccctccttg aggtccttcc 60

tccccaagcc cacctgggtg ccctctttct ccctgaggct ccacttggtc tctccgcgc 119

atg cct gcc ctg tgg ccc acc ctg gcc gct ctg gct ctg ctg agc agc 167
Met Pro Ala Leu Trp Pro Thr Leu Ala Ala Leu Ala Leu Leu Ser Ser
-95 -90 -85 -80

gtc gca gag gcc tcc ctg ggc tcc gcg ccc cgc agc cct gcc ccc cgc 215
Val Ala Glu Ala Ser Leu Gly Ser Ala Pro Arg Ser Pro Ala Pro Arg
-75 -70 -65

gaa ggc ccc ccg cct gtc ctg gcg tcc ccc gcc ggc cac ctg ccg ggg 263
Glu Gly Pro Pro Pro Val Leu Ala Ser Pro Ala Gly His Leu Pro Gly
-60 -55 -50

gga cgc acg gcc cgc tgg tgc agt gga aga gcc cgg cgg ccg cgc cgc 311
Gly Arg Thr Ala Arg Trp Cys Ser Gly Arg Ala Arg Arg Pro Arg Arg
-45 -40 -35

aga cac ttc tcg gcc cgc gcc ccc gcc gcc tgc acc ccc atc tgc tct 359
Arg His Phe Ser Ala Arg Ala Pro Ala Ala Cys Thr Pro Ile Cys Ser
-30 -25 -20

tcc ccg cgg gtc cgc gcg gcg cgg ctg ggg ggc cgg gca gcg cgc tcg 407
Ser Pro Arg Val Arg Ala Ala Arg Leu Gly Gly Arg Ala Ala Arg Ser
-15 -10 -5 -1 1

ggc agc ggg ggc gcg ggg tgc cgc ctg cgc tcg cag ctg gtg ccg gtg 455
Gly Ser Gly Gly Ala Gly Cys Arg Leu Arg Ser Gln Leu Val Pro Val
5 10 15

cgc gcg ctc ggc ctg ggc cac cgc tcc gac gag ctg gtg cgt ttc cgc 503
Arg Ala Leu Gly Leu Gly His Arg Ser Asp Glu Leu Val Arg Phe Arg
20 25 30

```

ttc tgc acc ggc tcc tgc ccg cgc gcg cgc tct cca cac gac ctc agc 551
 Phe Cys Thr Gly Ser Cys Pro Arg Ala Arg Ser Pro His Asp Leu Ser
 35 40 45
 ctg gcc agc cta ctg ggc gcc ggg gcc ctg cga ccg ccc ccg ggc tcc 599
 Leu Ala Ser Leu Leu Gly Ala Gly Ala Leu Arg Pro Pro Pro Gly Ser
 50 55 60 65
 cgg ccc gtc agc cag ccc tgc tgc cga ccc acg cgc tac gaa gcg gtc 647
 Arg Pro Val Ser Gln Pro Cys Cys Arg Pro Thr Arg Tyr Glu Ala Val
 70 75 80
 tcc ttc atg gac gtc aac agc acc tgg aga acc gtg gac cgc ctc tcc 695
 Ser Phe Met Ala Asp Val Asn Ser Thr Trp Arg Thr Val Asp Arg Leu Ser
 85 90 95
 gcc acc gcc tgc ggc tgc ctg ggc tgaggggctcg ctccaggggt ttgcagactg 749
 Ala Thr Ala Cys Gly Cys Leu Gly
 100 105
 gacccttacc ggtggctctt cctgcctggg accctcccgc agagtccac tagccagcgg 809
 cctcagccag ggacgaaggc ctcaaagctg agaggcccct gccggtgggt gatgga 865

<210> 2
 <211> 200
 <212> PRT
 <213> Homo sapiens

<400> 2
 Met Pro Ala Leu Trp Pro Thr Leu Ala Ala Leu Ala Leu Leu Ser Ser
 -95 -90 -85 -80
 Val Ala Glu Ala Ser Leu Gly Ser Ala Pro Arg Ser Pro Ala Pro Arg
 -75 -70 -65
 Glu Gly Pro Pro Pro Val Leu Ala Ser Pro Ala Gly His Leu Pro Gly
 -60 -55 -50
 Gly Arg Thr Ala Arg Trp Cys Ser Gly Arg Ala Arg Arg Pro Arg Arg
 -45 -40 -35
 Arg His Phe Ser Ala Arg Ala Pro Ala Ala Cys Thr Pro Ile Cys Ser
 -30 -25 -20
 Ser Pro Arg Val Arg Ala Ala Arg Leu Gly Gly Arg Ala Ala Arg Ser
 -15 -10 -5 -1 1
 Gly Ser Gly Gly Ala Gly Cys Arg Leu Arg Ser Gln Leu Val Pro Val
 5 10 15
 Arg Ala Leu Gly Leu Gly His Arg Ser Asp Glu Leu Val Arg Phe Arg
 20 25 30
 Phe Cys Thr Gly Ser Cys Pro Arg Ala Arg Ser Pro His Asp Leu Ser
 35 40 45
 Leu Ala Ser Leu Leu Gly Ala Gly Ala Leu Arg Pro Pro Pro Gly Ser
 50 55 60 65
 Arg Pro Val Ser Gln Pro Cys Cys Arg Pro Thr Arg Tyr Glu Ala Val
 70 75 80

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Phe | Met | Asp | Val | Asn | Ser | Thr | Trp | Arg | Thr | Val | Asp | Arg | Leu | Ser |
| | | | 85 | | | | | 90 | | | | | 95 | | |
| | | | | | | | | | | | | | | | |
| Ala | Thr | Ala | Cys | Gly | Cys | Leu | Gly | | | | | | | | |
| | | 100 | | | | | 105 | | | | | | | | |

<210> 3
 <211> 861
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (7)..(717)

<220>
 <221> 5'UTR
 <222> (1)..(6)

<220>
 <221> 3'UTR
 <222> (718)..(861)

<220>
 <221> sig_peptide
 <222> (7)..(174)

<220>
 <221> mat_peptide
 <222> (298)..(717)

<220>
 <221> mat_peptide
 <222> (370)..(717)

<220>
 <221> mat_peptide
 <222> (379)..(717)

<220>
 <221> misc_structure
 <222> (661)..(663)
 <223> CARBOHYD: glycosylated Asparagine as Asn122

<220>
 <221> misc_structure
 <222> (424)..(621)
 <223> DISULFID: Cys43-Cys108 disulfide bridge

<220>
 <221> misc_structure
 <222> (505)..(705)
 <223> DISULFID: Cys70-Cys136 disulfide bridge

<220>
 <221> misc_structure
 <222> (517)..(711)
 <223> DISULFID: Cys74-Cys138 disulfide bridge

<220>
 <221> misc_structure

<222> (616)..(618)

<223> DISULFID: Cys107-Cys107 interchain disulfide
bridge

<400> 3

| | |
|---|-----|
| gagccc atg ccc ggc ctg atc tca gcc cga gga cag ccc ctc ctt gag | 48 |
| Met Pro Gly Leu Ile Ser Ala Arg Gly Gln Pro Leu Leu Glu | |
| -95 -90 -85 | |
| gtc ctt cct ccc caa gcc cac ctg ggt gcc ctc ttt ctc cct gag gct | 96 |
| Val Leu Pro Pro Gln Ala His Leu Gly Ala Leu Phe Leu Pro Glu Ala | |
| -80 -75 -70 | |
| cca ctt ggt ctc tcc gcg cag cct gcc ctg tgg ccc acc ctg gcc gct | 144 |
| Pro Leu Gly Leu Ser Ala Gln Pro Ala Leu Trp Pro Thr Leu Ala Ala | |
| -65 -60 -55 | |
| ctg gct ctg ctg agc agc gtc gca gag gcc tcc ctg ggc tcc gcg ccc | 192 |
| Leu Ala Leu Leu Ser Ser Val Ala Glu Ala Ser Leu Gly Ser Ala Pro | |
| -50 -45 -40 | |
| cgc agc cct gcc ccc cgc gaa ggc ccc ccg cct gtc ctg gcg tcc ccc | 240 |
| Arg Ser Pro Ala Pro Arg Glu Gly Pro Pro Pro Val Leu Ala Ser Pro | |
| -35 -30 -25 -20 | |
| gcc ggc cac ctg ccg ggg gga cgc acg gcc cgc tgg tgc agt gga aga | 288 |
| Ala Gly His Leu Pro Gly Gly Arg Thr Ala Arg Trp Cys Ser Gly Arg | |
| -15 -10 -5 | |
| gcc cgg cgg ccg ccg ccg cag cct tct ccg ccc gcg ccc ccg ccg cct | 336 |
| Ala Arg Arg Pro Pro Pro Gln Pro Ser Arg Pro Ala Pro Pro Pro Pro | |
| -1 1 5 10 | |
| gca ccc cca tct gct ctt ccc cgc ggg ggc cgc gcg gcg cgg gct ggg | 384 |
| Ala Pro Pro Ser Ala Leu Pro Arg Gly Gly Arg Ala Ala Arg Ala Gly | |
| 15 20 25 | |
| ggc ccg ggc aac cgc gct ccg gca gcg ggg gcg ccg ggc tgc cgc ctg | 432 |
| Gly Pro Gly Asn Arg Ala Arg Ala Ala Gly Ala Arg Gly Cys Arg Leu | |
| 30 35 40 45 | |
| cgc tcg cag ctg gtg ccg gtg cgc gcg ctc ggc ctg ggc cac cgc tcc | 480 |
| Arg Ser Gln Leu Val Pro Val Arg Ala Leu Gly Leu Gly His Arg Ser | |
| 50 55 60 | |
| gac gag ctg gtg cgt ttc cgc ttc tgc agc ggc tcc tgc cgc cgc gcg | 528 |
| Asp Glu Leu Val Arg Phe Arg Phe Cys Ser Gly Ser Cys Arg Arg Ala | |
| 65 70 75 | |
| cgc tct cca cac gac ctc agc ctg gcc agc cta ctg ggc gcc ggg gcc | 576 |
| Arg Ser Pro His Asp Leu Ser Leu Ala Ser Leu Leu Gly Ala Gly Ala | |
| 80 85 90 | |
| ctg cga ccg ccc ccg ggc tcc ccg ccc gtc agc cag ccc tgc tgc cga | 624 |
| Leu Arg Pro Pro Pro Gly Ser Arg Pro Val Ser Gln Pro Cys Cys Arg | |
| 95 100 105 | |
| ccc acg cgc tac gaa gcg gtc tcc ttc atg gac gtc aac agc acc tgg | 672 |
| Pro Thr Arg Tyr Glu Ala Val Ser Phe Met Asp Val Asn Ser Thr Trp | |
| 110 115 120 125 | |
| aga acc gtg gac cgc ctc tcc gcc aac ccc tgc ggc tgc ctg ggc | 717 |
| Arg Thr Val Asp Arg Leu Ser Ala Asn Pro Cys Gly Cys Leu Gly | |
| 130 135 140 | |

<213> Homo sapiens

<220>

<223> Wherein Xaa at position 134 designates Asn or Thr,
and Xaa at position 135 designates Ala or Pro

<400> 5

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Pro | Pro | Pro | Gln | Pro | Ser | Arg | Pro | Ala | Pro | Pro | Pro | Pro | Ala | Pro | Pro |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Ser | Ala | Leu | Pro | Arg | Gly | Gly | Arg | Ala | Ala | Arg | Ala | Gly | Gly | Pro | Gly |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Asn | Arg | Ala | Arg | Ala | Ala | Gly | Ala | Arg | Gly | Cys | Arg | Leu | Arg | Ser | Gln |
| | | 35 | | | | | 40 | | | | | 45 | | | |
| Leu | Val | Pro | Val | Arg | Ala | Leu | Gly | Leu | Gly | His | Arg | Ser | Asp | Glu | Leu |
| | 50 | | | | | 55 | | | | | 60 | | | | |
| Val | Arg | Phe | Arg | Phe | Cys | Ser | Gly | Ser | Cys | Arg | Arg | Ala | Arg | Ser | Pro |
| 65 | | | | | 70 | | | | 75 | | | | | | 80 |
| His | Asp | Leu | Ser | Leu | Ala | Ser | Leu | Leu | Gly | Ala | Gly | Ala | Leu | Arg | Pro |
| | | | 85 | | | | | | 90 | | | | | 95 | |
| Pro | Pro | Gly | Ser | Arg | Pro | Val | Ser | Gln | Pro | Cys | Cys | Arg | Pro | Thr | Arg |
| | | | 100 | | | | | 105 | | | | | 110 | | |
| Tyr | Glu | Ala | Val | Ser | Phe | Met | Asp | Val | Asn | Ser | Thr | Trp | Arg | Thr | Val |
| | 115 | | | | | | 120 | | | | | 125 | | | |
| Asp | Arg | Leu | Ser | Ala | Xaa | Xaa | Cys | Gly | Cys | Leu | Gly | | | | |
| | 130 | | | | | 135 | | | | | 140 | | | | |

<210> 6

<211> 116

<212> PRT

<213> Homo sapiens

<220>

<223> Wherein Xaa at position 110 designates Asn or Thr,
and Xaa at position 111 designates Ala or Pro

<400> 6

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Ala | Arg | Ala | Gly | Gly | Pro | Gly | Asn | Arg | Ala | Arg | Ala | Ala | Gly | Ala |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Arg | Gly | Cys | Arg | Leu | Arg | Ser | Gln | Leu | Val | Pro | Val | Arg | Ala | Leu | Gly |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Leu | Gly | His | Arg | Ser | Asp | Glu | Leu | Val | Arg | Phe | Arg | Phe | Cys | Ser | Gly |
| | | 35 | | | | | 40 | | | | | 45 | | | |
| Ser | Cys | Arg | Arg | Ala | Arg | Ser | Pro | His | Asp | Leu | Ser | Leu | Ala | Ser | Leu |
| | 50 | | | | | 55 | | | | 60 | | | | | |
| Leu | Gly | Ala | Gly | Ala | Leu | Arg | Pro | Pro | Pro | Gly | Ser | Arg | Pro | Val | Ser |
| 65 | | | | | 70 | | | | | 75 | | | | | 80 |
| Gln | Pro | Cys | Cys | Arg | Pro | Thr | Arg | Tyr | Glu | Ala | Val | Ser | Phe | Met | Asp |
| | | | | 85 | | | | | 90 | | | | | 95 | |
| Val | Asn | Ser | Thr | Trp | Arg | Thr | Val | Asp | Arg | Leu | Ser | Ala | Xaa | Xaa | Cys |

100 105 110
 Gly Cys Leu Gly
 115

 <210> 7
 <211> 113
 <212> PRT
 <213> Homo sapiens

 <220>
 <223> Wherein Xaa at position 107 designates Asn or Thr,
 and Xaa at position 108 designates Ala or Pro

 <400> 7
 Ala Gly Gly Pro Gly Asn Arg Ala Arg Ala Ala Gly Ala Arg Gly Cys
 1 5 10 15
 Arg Leu Arg Ser Gln Leu Val Pro Val Arg Ala Leu Gly Leu Gly His
 20 25 30
 Arg Ser Asp Glu Leu Val Arg Phe Arg Phe Cys Ser Gly Ser Cys Arg
 35 40 45
 Arg Ala Arg Ser Pro His Asp Leu Ser Leu Ala Ser Leu Leu Gly Ala
 50 55 60
 Gly Ala Leu Arg Pro Pro Pro Gly Ser Arg Pro Val Ser Gln Pro Cys
 65 70 75 80
 Cys Arg Pro Thr Arg Tyr Glu Ala Val Ser Phe Met Asp Val Asn Ser
 85 90 95
 Thr Trp Arg Thr Val Asp Arg Leu Ser Ala Xaa Xaa Cys Gly Cys Leu
 100 105 110

Gly

<210> 8
 <211> 861
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (58)..(717)

<220>
 <221> 5'UTR
 <222> (1)..(57)

<220>
 <221> 3'UTR
 <222> (718)..(861)

<220>
 <221> sig_peptide
 <222> (58)..(174)

<220>
 <221> mat_peptide

<222> (298)..(717)

<220>

<221> mat_peptide

<222> (370)..(717)

<220>

<221> mat_peptide

<222> (379)..(717)

<220>

<221> misc_structure

<222> (661)..(663)

<223> CARBOHYD: glycosylated asparagine at Asn122

<220>

<221> misc_structure

<222> (424)..(621)

<223> DISULFID: Gly43-Gly108 disulfide bridge

<220>

<221> misc_structure

<222> (505)..(705)

<223> DISULFID: Gly70-Gly136 disulfide bridge

<220>

<221> misc_structure

<222> (517)..(711)

<223> DISULFID: Gly74-Gly138 disulfide bridge

<220>

<221> misc_structure

<222> (616)..(618)

<223> DISULFID: Gly107-Gly107 interchain disulfide
bridge

<400> 8

aggagggtgg gggaacagct caacaatggc tgatgggcgc tcctggtgtt gatagag 57

atg gaa ctt gga ctt gga ggc ctc tcc acg ctg tcc cac tgc ccc tgg 105
Met Glu Leu Gly Leu Gly Gly Leu Ser Thr Leu Ser His Cys Pro Trp
-80 -75 -70 -65

cct agg cgg cag cct gcc ctg tgg ccc acc ctg gcc gct ctg gct ctg 153
Pro Arg Arg Gln Pro Ala Leu Trp Pro Thr Leu Ala Ala Leu Ala Leu
-60 -55 -50

ctg agc agc gtc gca gag gcc tcc ctg ggc tcc gcg ccc cgc agc cct 201
Leu Ser Ser Val Ala Glu Ala Ser Leu Gly Ser Ala Pro Arg Ser Pro
-45 -40 -35

gcc ccc cgc gaa ggc ccc ccg cct gtc ctg gcg tcc ccc gcc ggc cac 249
Ala Pro Arg Glu Gly Pro Pro Pro Val Leu Ala Ser Pro Ala Gly His
-30 -25 -20

ctg ccg ggg gga cgc acg gcc cgc tgg tgc agt gga aga gcc cgg cgg 297
Leu Pro Gly Gly Arg Thr Ala Arg Trp Cys Ser Gly Arg Ala Arg Arg
-15 -10 -5 -1

ccg ccg ccg cag cct tct cgg ccc gcg ccc ccg ccg cct gca ccc cca 345
Pro Pro Pro Gln Pro Ser Arg Pro Ala Pro Pro Pro Pro Ala Pro Pro
1 5 10 15

tct gct ctt ccc cgc ggg ggc cgc gcg gcg cgg gct ggg ggc ccg ggc 393

Ser Ala Leu Pro Arg Gly Gly Arg Ala Ala Arg Ala Gly Gly Pro Gly
 20 25 30
 agc cgc gct cgg gca gcg ggg gcg cgg ggc tgc cgc ctg cgc tcg cag 441
 Ser Arg Ala Arg Ala Ala Gly Ala Arg Gly Cys Arg Leu Arg Ser Gln
 35 40 45
 ctg gtg ccg gtg cgc gcg ctc ggc ctg ggc cac cgc tcc gac gag ctg 489
 Leu Val Pro Val Arg Ala Leu Gly Leu Gly His Arg Ser Asp Glu Leu
 50 55 60
 gtg cgt ttc cgc ttc tgc agc ggc tcc tgc cgc cgc gcg cgc tct cca 537
 Val Arg Phe Arg Phe Cys Ser Gly Ser Cys Arg Arg Ala Arg Ser Pro
 65 70 75 80
 cac gac ctc agc ctg gcc agc cta ctg ggc gcc ggg gcc ctg cga ccg 585
 His Asp Leu Ser Leu Ala Ser Leu Leu Gly Ala Gly Ala Leu Arg Pro
 85 90 95
 ccc ccg ggc tcc cgg ccc gtc agc cag ccc tgc tgc cga ccc acg cgc 633
 Pro Pro Gly Ser Arg Pro Val Ser Gln Pro Cys Cys Arg Pro Thr Arg
 100 105 110
 tac gaa gcg gtc tcc ttc atg gac gtc aac agc acc tgg aga acc gtg 681
 Tyr Glu Ala Val Ser Phe Met Asp Val Asn Ser Thr Trp Arg Thr Val
 115 120 125
 gac cgc ctc tcc gcc acc gcc tgc ggc tgc ctg ggc tgagggctcg 727
 Asp Arg Leu Ser Ala Thr Ala Cys Gly Cys Leu Gly
 130 135 140
 ctccaggggt ttgcagactg gacccttacc ggtggctctt cctgcctggg accctcccgc 787
 agagtcccac tagccagcgg cctcagccag ggacgaaggc ctcaaagctg agaggcccct 847
 accggtgggt gatg 861

<210> 9
 <211> 220
 <212> PRT
 <213> Homo sapiens

<400> 9
 Met Glu Leu Gly Leu Gly Gly Leu Ser Thr Leu Ser His Cys Pro Trp
 -80 -75 -70 -65
 Pro Arg Arg Gln Pro Ala Leu Trp Pro Thr Leu Ala Ala Leu Ala Leu
 -60 -55 -50
 Leu Ser Ser Val Ala Glu Ala Ser Leu Gly Ser Ala Pro Arg Ser Pro
 -45 -40 -35
 Ala Pro Arg Glu Gly Pro Pro Pro Val Leu Ala Ser Pro Ala Gly His
 -30 -25 -20
 Leu Pro Gly Gly Arg Thr Ala Arg Trp Cys Ser Gly Arg Ala Arg Arg
 -15 -10 -5 -1
 Pro Pro Pro Gln Pro Ser Arg Pro Ala Pro Pro Pro Pro Ala Pro Pro
 1 5 10 15
 Ser Ala Leu Pro Arg Gly Gly Arg Ala Ala Arg Ala Gly Gly Pro Gly
 20 25 30

Ser Arg Ala Arg Ala Ala Gly Ala Arg Gly Cys Arg Leu Arg Ser Gln
 35 40 45
 Leu Val Pro Val Arg Ala Leu Gly Leu Gly His Arg Ser Asp Glu Leu
 50 55 60
 Val Arg Phe Arg Phe Cys Ser Gly Ser Cys Arg Arg Ala Arg Ser Pro
 65 70 75 80
 His Asp Leu Ser Leu Ala Ser Leu Leu Gly Ala Gly Ala Leu Arg Pro
 85 90 95
 Pro Pro Gly Ser Arg Pro Val Ser Gln Pro Cys Cys Arg Pro Thr Arg
 100 105 110
 Tyr Glu Ala Val Ser Phe Met Asp Val Asn Ser Thr Trp Arg Thr Val
 115 120 125
 Asp Arg Leu Ser Ala Thr Ala Cys Gly Cys Leu Gly
 130 135 140

<210> 10
 <211> 140
 <212> PRT
 <213> Homo sapiens

<220>
 <221> CARBOHYD
 <222> (122)
 <223> glycosylated asparagine

<400> 10
 Pro Pro Pro Gln Pro Ser Arg Pro Ala Pro Pro Pro Pro Ala Pro Pro
 1 5 10 15
 Ser Ala Leu Pro Arg Gly Gly Arg Ala Ala Arg Ala Gly Gly Pro Gly
 20 25 30
 Ser Arg Ala Arg Ala Ala Gly Ala Arg Gly Cys Arg Leu Arg Ser Gln
 35 40 45
 Leu Val Pro Val Arg Ala Leu Gly Leu Gly His Arg Ser Asp Glu Leu
 50 55 60
 Val Arg Phe Arg Phe Cys Ser Gly Ser Cys Arg Arg Ala Arg Ser Pro
 65 70 75 80
 His Asp Leu Ser Leu Ala Ser Leu Leu Gly Ala Gly Ala Leu Arg Pro
 85 90 95
 Pro Pro Gly Ser Arg Pro Val Ser Gln Pro Cys Cys Arg Pro Thr Arg
 100 105 110
 Tyr Glu Ala Val Ser Phe Met Asp Val Asn Ser Thr Trp Arg Thr Val
 115 120 125
 Asp Arg Leu Ser Ala Thr Ala Cys Gly Cys Leu Gly
 130 135 140

<210> 11

<211> 116
<212> PRT
<213> Homo sapiens

<220>
<221> CARBOHYD
<222> (98)
<223> glycosylated asparagine

<400> 11
Ala Ala Arg Ala Gly Gly Pro Gly Ser Arg Ala Arg Ala Ala Gly Ala
1 5 10 15
Arg Gly Cys Arg Leu Arg Ser Gln Leu Val Pro Val Arg Ala Leu Gly
20 25 30
Leu Gly His Arg Ser Asp Glu Leu Val Arg Phe Arg Phe Cys Ser Gly
35 40 45
Ser Cys Arg Arg Ala Arg Ser Pro His Asp Leu Ser Leu Ala Ser Leu
50 55 60
Leu Gly Ala Gly Ala Leu Arg Pro Pro Pro Gly Ser Arg Pro Val Ser
65 70 75 80
Gln Pro Cys Cys Arg Pro Thr Arg Tyr Glu Ala Val Ser Phe Met Asp
85 90 95
Val Asn Ser Thr Trp Arg Thr Val Asp Arg Leu Ser Ala Thr Ala Cys
100 105 110
Gly Cys Leu Gly
115

<210> 12
<211> 113
<212> PRT
<213> Homo sapiens

<220>
<221> CARBOHYD
<222> (95)
<223> glycosylated asparagine

<400> 12
Ala Gly Gly Pro Gly Ser Arg Ala Arg Ala Ala Gly Ala Arg Gly Cys
1 5 10 15
Arg Leu Arg Ser Gln Leu Val Pro Val Arg Ala Leu Gly Leu Gly His
20 25 30
Arg Ser Asp Glu Leu Val Arg Phe Arg Phe Cys Ser Gly Ser Cys Arg
35 40 45
Arg Ala Arg Ser Pro His Asp Leu Ser Leu Ala Ser Leu Leu Gly Ala
50 55 60
Gly Ala Leu Arg Pro Pro Pro Gly Ser Arg Pro Val Ser Gln Pro Cys
65 70 75 80
Cys Arg Pro Thr Arg Tyr Glu Ala Val Ser Phe Met Asp Val Asn Ser
85 90 95

Thr Trp Arg Thr Val Asp Arg Leu Ser Ala Thr Ala Cys Gly Cys Leu
100 105 110

Gly

<210> 13
<211> 102
<212> DNA
<213> Homo sapiens

<400> 13
cctggccagc ctactgggcg ccgggggccct gcgaccgccc ccgggctccc ggcccgtcag 60
ccagccctgc tgccgaccca cgcgctacga agcggctctc tt 102

<210> 14
<211> 220
<212> DNA
<213> Murinae gen. sp.

<400> 14
ggccaccgct ccgacgagct gatacgtttc cgcttctgca gcggtctcgtg ccgccgagca 60
cgctcccagc acgatctcag tctggccagc ctactgggcg ctggggccct acggtcgcct 120
cccgggtccc ggccgatcag ccagccctgc tgccggccca ctcgctatga ggccgtctcc 180
ttcatggacg tgaacagcac ctggagaacc gtggaccgcc 220

<210> 15
<211> 2136
<212> DNA
<213> Murinae gen. sp.

<220>
<221> CDS
<222> (975)..(1646)

<400> 15
gcgccgcgca attcggcacg agggcgctctc gctgcagccc gcgatctcta ctctgcctcc 60
tggggctcttc tccaaatgtc tagccccac ctagagggac ctagcctagc cagcggggac 120
cggatccgga ggggtggagcg gccagggtgag ccctgaaagg tggggcgggg cgggggcgct 180
ctggggccca ccccgggatc tgggtgacgcc ggggctggaa tttgacaccg gacggcgggc 240
ggcaggaggc tgctgaggga tggagttggg ctcgggcccc agatgcggcc cgcgggctct 300
gccagcaaca agtcctctcg gccccagccc tcgctgcgac tggggcttgg agccctgcac 360
ccaagggcac agaccggctg ccaaggcccc acttttaact aaaagaggcg ctgccagggtg 420
cacaactctg ggcatgatcc acttgagctt cgggggaaag ccagcactg gtcccaggag 480
aggcgcctag aaggacacgg accaggaccc ctttggtatg gagtgaacgc tgagcatgga 540
gtggaaggaa ctcaagttac tactttctcc aaccaccctg gtaccttcag ccctgaagta 600
cagagcagaa gggctcttaga agacaggacc acagctgtgt gagtctcccc cctgaggcct 660
tagacgatct ctgagctcag ctgagctttg tttgcccatc tggagaagtg agccattgat 720
tgaccttgtg gcacgcgcaa ggaacaggtc ctgccaaagca cctaacacag agagcaaggt 780

| | |
|---|------|
| tctccatcgc agctaccgct gctgagttga ctctagctac tccaacctcc tgggtcgctt | 840 |
| cgagagactg gagtggaagg aggaataccc caaaggataa ctaactcatc tttcagtttg | 900 |
| caagctgccg caggaagagg gtgggggaaac ggggtccacga aggcttctga tgggagcttc | 960 |
| tggagccgaa agct atg gaa ctg gga ctt gca gag cct act gca ttg tcc | 1010 |
| Met Glu Leu Gly Leu Ala Glu Pro Thr Ala Leu Ser | |
| 1 5 10 | |
| cac tgc ctc cgg cct agg tgg cag tca gcc tgg tgg cca acc cta gct | 1058 |
| His Cys Leu Arg Pro Arg Trp Gln Ser Ala Trp Trp Pro Thr Leu Ala | |
| 15 20 25 | |
| gtt cta gcc ctg ctg agc tgc gtc aca gaa gct tcc ctg gac cca atg | 1106 |
| Val Leu Ala Leu Leu Ser Cys Val Thr Glu Ala Ser Leu Asp Pro Met | |
| 30 35 40 | |
| tcc cgc agc ccc gcc gct cgc gac ggt ccc tca ccg gtc ttg gcg ccc | 1154 |
| Ser Arg Ser Pro Ala Ala Arg Asp Gly Pro Ser Pro Val Leu Ala Pro | |
| 45 50 55 60 | |
| ccc acg gac cac ctg cct ggg gga cac act gcg cat ttg tgc agc gaa | 1202 |
| Pro Thr Asp His Leu Pro Gly Gly His Thr Ala His Leu Cys Ser Glu | |
| 65 70 75 | |
| aga acc ctg cga ccc ccg cct cag tct cct cag ccc gca ccc ccg ccg | 1250 |
| Arg Thr Leu Arg Pro Pro Pro Gln Ser Pro Gln Pro Ala Pro Pro Pro | |
| 80 85 90 | |
| cct ggt ccc gcg ctc cag tct cct ccc gct gcg ctc cgc ggg gca cgc | 1298 |
| Pro Gly Pro Ala Leu Gln Ser Pro Pro Ala Ala Leu Arg Gly Ala Arg | |
| 95 100 105 | |
| gcg gcg cgt gca gga acc ccg agc agc cgc gca ccg acc aca gat gcg | 1346 |
| Ala Ala Arg Ala Gly Thr Arg Ser Ser Arg Ala Arg Thr Thr Asp Ala | |
| 110 115 120 | |
| cgc ggc tgc cgc ctg cgc tgc cag ctg gtg ccg gtg agc gcg ctc ggc | 1394 |
| Arg Gly Cys Arg Leu Arg Ser Gln Leu Val Pro Val Ser Ala Leu Gly | |
| 125 130 135 140 | |
| cta ggc cac agc tcc gac gag ctg ata cgt ttc cgc ttc tgc agc ggc | 1442 |
| Leu Gly His Ser Ser Asp Glu Leu Ile Arg Phe Arg Phe Cys Ser Gly | |
| 145 150 155 | |
| tgc tgc cgc cga gca cgc tcc cag cac gat ctc agt ctg gcc agc cta | 1490 |
| Ser Cys Arg Arg Ala Arg Ser Gln His Asp Leu Ser Leu Ala Ser Leu | |
| 160 165 170 | |
| ctg ggc gct ggg gcc cta ccg tgc cct ccc ggg tcc ccg ccg atc agc | 1538 |
| Leu Gly Ala Gly Ala Leu Arg Ser Pro Pro Gly Ser Arg Pro Ile Ser | |
| 175 180 185 | |
| cag ccc tgc tgc ccg ccc act cgc tat gag gcc gtc tcc ttc atg gac | 1586 |
| Gln Pro Cys Cys Arg Pro Thr Arg Tyr Glu Ala Val Ser Phe Met Asp | |
| 190 195 200 | |
| gtg aac agc acc tgg agg acc gtg gac cac ctc tcc gcc act gcc tgc | 1634 |
| Val Asn Ser Thr Trp Arg Thr Val Asp His Leu Ser Ala Thr Ala Cys | |
| 205 210 215 220 | |
| ggc tgt ctg ggc tgaggatgat ctatctccaa gcctttgcac actagaccca | 1686 |

Gly Cys Leu Gly

tgtgttgccc tacctggaac agctccaccg ggcctcacta accaggagcc tcaactcagc 1746
aggatatgga ggctgcagag ctcaggcccc aggccggtga gtgacagacg tcgtcggcat 1806
gacagacaga gtgaaagatg tcggaaccac tgaccaacag tcccaagttg ttcattggatc 1866
ccagctctac agacaggaga aacctcagct aaagagaact cctctgggag aatccagaaa 1926
tggccctctg tcttggggaa tgaattttga agagatatat atacatatat acattgtagt 1986
cgcgttgctg gaccagcctg tgctgaaacc agtcccgtgt tcacttgtgg aagccgaagc 2046
cctatttatt atttctaaat tattttattta ctttgaaaaa aaacggccaa gtcggcctcc 2106
ctttagttag gggttaatttg tgatcccggg 2136

<210> 16
<211> 224
<212> PRT
<213> Murinae gen. sp.

<400> 16
Met Glu Leu Gly Leu Ala Glu Pro Thr Ala Leu Ser His Cys Leu Arg
1 5 10 15
Pro Arg Trp Gln Ser Ala Trp Trp Pro Thr Leu Ala Val Leu Ala Leu
20 25 30
Leu Ser Cys Val Thr Glu Ala Ser Leu Asp Pro Met Ser Arg Ser Pro
35 40 45
Ala Ala Arg Asp Gly Pro Ser Pro Val Leu Ala Pro Pro Thr Asp His
50 55 60
Leu Pro Gly Gly His Thr Ala His Leu Cys Ser Glu Arg Thr Leu Arg
65 70 75 80
Pro Pro Pro Gln Ser Pro Gln Pro Ala Pro Pro Pro Gly Pro Ala
85 90 95
Leu Gln Ser Pro Pro Ala Ala Leu Arg Gly Ala Arg Ala Ala Arg Ala
100 105 110
Gly Thr Arg Ser Ser Arg Ala Arg Thr Thr Asp Ala Arg Gly Cys Arg
115 120 125
Leu Arg Ser Gln Leu Val Pro Val Ser Ala Leu Gly Leu Gly His Ser
130 135 140
Ser Asp Glu Leu Ile Arg Phe Arg Phe Cys Ser Gly Ser Cys Arg Arg
145 150 155 160
Ala Arg Ser Gln His Asp Leu Ser Leu Ala Ser Leu Leu Gly Ala Gly
165 170 175
Ala Leu Arg Ser Pro Pro Gly Ser Arg Pro Ile Ser Gln Pro Cys Cys
180 185 190
Arg Pro Thr Arg Tyr Glu Ala Val Ser Phe Met Asp Val Asn Ser Thr
195 200 205

Trp Arg Thr Val Asp His Leu Ser Ala Thr Ala Cys Gly Cys Leu Gly
 210 215 220

<210> 17
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: PCR Primer

<400> 17
 cctggccagc ctactggg 18

<210> 18
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: PCR Primer

<400> 18
 aaggagaccg cttcgtagcg 20

<210> 19
 <211> 17
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: PCR Primer

<400> 19
 atggaacttg gacttgg 17

<210> 20
 <211> 16
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: PCR Primer

<400> 20
 tccatcaccc accggc 16

<210> 21
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: PCR Primer

<400> 21
 ggccaccgct ccgacgag 18

<210> 22
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: PCR Primer

 <400> 22
 ggcggtccac ggttctccag 20

 <210> 23
 <211> 29
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: PCR Primer

 <400> 23
 ccaagcccac ctgggtgccc tctttctcc 29

 <210> 24
 <211> 27
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: PCR Primer

 <400> 24
 catcaccac cggcaggggc ctctcag 27

 <210> 25
 <211> 35
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: PCR Primer

 <400> 25
 gagcccatgc ccggcctgat ctcagcccga ggaca 35

 <210> 26
 <211> 34
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: PCR Primer

 <400> 26
 ccctggctga ggccgctggc tagtgggact ctgc 34

 <210> 27
 <211> 31
 <212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Hybridization Probe

<220>

<221> misc_structure

<222> (1)

<223> wherein n represents a conjugant moiety linking to alkaline phosphatase

<400> 27

ncaggtggtc cgtggggggc gccaaagaccg g

31

<210> 28

<211> 16

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR primer

<400> 28

ctaggagccc atgccc

16

<210> 29

<211> 351

<212> DNA

<213> Homo sapiens

<400> 29

atggctggag gaccgggac tcgtgctcgt gcagcaggag cacgtggctg tcgtctgcgt 60
tctcaactag tgccggtgcg tgcactcgga ctgggacacc gttccgacga actagtagct 120
tttcgttttt gtccaggatc ttgtcgtcgt gcacgtttct cgcattgatc atctctagca 180
tctctactag gagccggagc actaagaccg ccgcccggat ctagacctgt atctcaacct 240
tgttgtagac ctactagata cgaagcagta tctttcatgg acgtaaactc tacatggaga 300
accgtagata gactatctgc aaccgcatgt ggctgtctag gatgataata g 351

<210> 30

<211> 414

<212> DNA

<213> Homo sapiens

<400> 30

atgggccatc atcatcatca tcatcatcat catcactcga gcggccatat cgacgacgac 60
gacaaggctg gaggaccggg atctcgtgct cgtgcagcag gagcacgtgg ctgtcgtctg 120
cgttctcaac tagtgccggt gcgtgcactc ggactgggac accgttccga cgaactagta 180
cgttttcgtt ttgtttcagg atcttgctgt cgtgcacgtt ctccgcatga tctatctcta 240
gcatctctac taggagccgg agcactaaga ccgcccggcg gatctagacc tgtatctcaa 300
ccttgttgta gacctactag atacgaagca gtatctttca tggacgtaaa ctctacatgg 360
agaaccgtag atagactatc tgcaaccgca tgtggctgtc taggatgata atag 414

<210> 31

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR primer

<400> 31
aaggaaaaaa gcggccgcca tggaacttgg acttggagg 39

<210> 32
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR primer

<400> 32
ttttttcctt ggcggccgct cagcccaggc agccgcagg 39

<210> 33
<211> 16
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 33
gagcgagccc tcagcc 16

<210> 34
<211> 224
<212> PRT
<213> Rattus sp.

<400> 34
Met Glu Leu Gly Leu Gly Glu Pro Thr Ala Leu Ser His Cys Leu Arg
1 5 10 15
Pro Arg Trp Gln Pro Ala Leu Trp Pro Thr Leu Ala Ala Leu Ala Leu
20 25 30
Leu Ser Ser Val Thr Glu Ala Ser Leu Asp Pro Met Ser Arg Ser Pro
35 40 45
Ala Ser Arg Asp Val Pro Ser Pro Val Leu Ala Pro Pro Thr Asp Tyr
50 55 60
Leu Pro Gly Gly His Thr Ala His Leu Cys Ser Glu Arg Ala Leu Arg
65 70 75 80
Pro Pro Pro Gln Ser Pro Gln Pro Ala Pro Pro Pro Pro Gly Pro Ala
85 90 95
Leu Gln Ser Pro Pro Ala Ala Leu Arg Gly Ala Arg Ala Ala Arg Ala
100 105 110
Gly Thr Arg Ser Ser Arg Ala Arg Ala Thr Asp Ala Arg Gly Cys Arg
115 120 125
Leu Arg Ser Gln Leu Val Pro Val Ser Ala Leu Gly Leu Gly His Ser
130 135 140
Ser Asp Glu Leu Ile Arg Phe Arg Phe Cys Ser Gly Ser Cys Arg Arg
145 150 155 160

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Arg | Ser | Pro | His | Asp | Leu | Ser | Leu | Ala | Ser | Leu | Leu | Gly | Ala | Gly |
| | | | | 165 | | | | | 170 | | | | | 175 | |
| Ala | Leu | Arg | Ser | Pro | Pro | Gly | Ser | Arg | Pro | Ile | Ser | Gln | Pro | Cys | Cys |
| | | | 180 | | | | | 185 | | | | | 190 | | |
| Arg | Pro | Thr | Arg | Tyr | Glu | Ala | Val | Ser | Phe | Met | Asp | Val | Asn | Ser | Thr |
| | | 195 | | | | | 200 | | | | | 205 | | | |
| Trp | Arg | Thr | Val | Asp | His | Leu | Ser | Ala | Thr | Ala | Cys | Gly | Cys | Leu | Gly |
| | 210 | | | | | 215 | | | | | 220 | | | | |

<210> 35
 <211> 112
 <212> PRT
 <213> Homo sapiens

| | | | | | | | | | | | | | | | |
|----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| <400> 35 | | | | | | | | | | | | | | | |
| Gly | Gly | Pro | Gly | Ser | Arg | Ala | Arg | Ala | Ala | Gly | Ala | Arg | Gly | Cys | Arg |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Leu | Arg | Ser | Gln | Leu | Val | Pro | Val | Arg | Ala | Leu | Gly | Leu | Gly | His | Arg |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Ser | Asp | Glu | Leu | Val | Arg | Phe | Arg | Phe | Cys | Ser | Gly | Ser | Cys | Arg | Arg |
| | | 35 | | | | | 40 | | | | | 45 | | | |
| Ala | Arg | Ser | Pro | His | Asp | Leu | Ser | Leu | Ala | Ser | Leu | Leu | Gly | Ala | Gly |
| | | 50 | | | | 55 | | | | | 60 | | | | |
| Ala | Leu | Arg | Pro | Pro | Pro | Gly | Ser | Arg | Pro | Val | Ser | Gln | Pro | Cys | Cys |
| | 65 | | | | 70 | | | | | 75 | | | | 80 | |
| Arg | Pro | Thr | Arg | Tyr | Glu | Ala | Val | Ser | Phe | Met | Asp | Val | Asn | Ser | Thr |
| | | | | 85 | | | | | 90 | | | | | 95 | |
| Trp | Arg | Thr | Val | Asp | Arg | Leu | Ser | Ala | Thr | Ala | Cys | Gly | Cys | Leu | Gly |
| | | | 100 | | | | | 105 | | | | | 110 | | |

<210> 36
 <211> 111
 <212> PRT
 <213> Homo sapiens

| | | | | | | | | | | | | | | | |
|----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| <400> 36 | | | | | | | | | | | | | | | |
| Gly | Pro | Gly | Ser | Arg | Ala | Arg | Ala | Ala | Gly | Ala | Arg | Gly | Cys | Arg | Leu |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Arg | Ser | Gln | Leu | Val | Pro | Val | Arg | Ala | Leu | Gly | Leu | Gly | His | Arg | Ser |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Asp | Glu | Leu | Val | Arg | Phe | Arg | Phe | Cys | Ser | Gly | Ser | Cys | Arg | Arg | Ala |
| | | 35 | | | | | 40 | | | | | 45 | | | |
| Arg | Ser | Pro | His | Asp | Leu | Ser | Leu | Ala | Ser | Leu | Leu | Gly | Ala | Gly | Ala |

50 55 60
 Leu Arg Pro Pro Pro Gly Ser Arg Pro Val Ser Gln Pro Cys Cys Arg
 65 70 75 80
 Pro Thr Arg Tyr Glu Ala Val Ser Phe Met Asp Val Asn Ser Thr Trp
 85 90 95
 Arg Thr Val Asp Arg Leu Ser Ala Thr Ala Cys Gly Cys Leu Gly
 100 105 110

<210> 37
 <211> 110
 <212> PRT
 <213> Homo sapiens

<400> 37
 Pro Gly Ser Arg Ala Arg Ala Ala Gly Ala Arg Gly Cys Arg Leu Arg
 1 5 10 15
 Ser Gln Leu Val Pro Val Arg Ala Leu Gly Leu Gly His Arg Ser Asp
 20 25 30
 Glu Leu Val Arg Phe Arg Phe Cys Ser Gly Ser Cys Arg Arg Ala Arg
 35 40 45
 Ser Pro His Asp Leu Ser Leu Ala Ser Leu Leu Gly Ala Gly Ala Leu
 50 55 60
 Arg Pro Pro Pro Gly Ser Arg Pro Val Ser Gln Pro Cys Cys Arg Pro
 65 70 75 80
 Thr Arg Tyr Glu Ala Val Ser Phe Met Asp Val Asn Ser Thr Trp Arg
 85 90 95
 Thr Val Asp Arg Leu Ser Ala Thr Ala Cys Gly Cys Leu Gly
 100 105 110

<210> 38
 <211> 109
 <212> PRT
 <213> Homo sapiens

<400> 38
 Gly Ser Arg Ala Arg Ala Ala Gly Ala Arg Gly Cys Arg Leu Arg Ser
 1 5 10 15
 Gln Leu Val Pro Val Arg Ala Leu Gly Leu Gly His Arg Ser Asp Glu
 20 25 30
 Leu Val Arg Phe Arg Phe Cys Ser Gly Ser Cys Arg Arg Ala Arg Ser
 35 40 45
 Pro His Asp Leu Ser Leu Ala Ser Leu Leu Gly Ala Gly Ala Leu Arg
 50 55 60
 Pro Pro Pro Gly Ser Arg Pro Val Ser Gln Pro Cys Cys Arg Pro Thr
 65 70 75 80
 Arg Tyr Glu Ala Val Ser Phe Met Asp Val Asn Ser Thr Trp Arg Thr
 85 90 95

Val Asp Arg Leu Ser Ala Thr Ala Cys Gly Cys Leu Gly
100 105

<210> 39
<211> 108
<212> PRT
<213> Homo sapiens

<400> 39
Ser Arg Ala Arg Ala Ala Gly Ala Arg Gly Cys Arg Leu Arg Ser Gln
1 5 10 15
Leu Val Pro Val Arg Ala Leu Gly Leu Gly His Arg Ser Asp Glu Leu
20 25 30
Val Arg Phe Arg Phe Cys Ser Gly Ser Cys Arg Arg Ala Arg Ser Pro
35 40 45
His Asp Leu Ser Leu Ala Ser Leu Leu Gly Ala Gly Ala Leu Arg Pro
50 55 60
Pro Pro Gly Ser Arg Pro Val Ser Gln Pro Cys Cys Arg Pro Thr Arg
65 70 75 80
Tyr Glu Ala Val Ser Phe Met Asp Val Asn Ser Thr Trp Arg Thr Val
85 90 95
Asp Arg Leu Ser Ala Thr Ala Cys Gly Cys Leu Gly
100 105

<210> 40
<211> 107
<212> PRT
<213> Homo sapiens

<400> 40
Arg Ala Arg Ala Ala Gly Ala Arg Gly Cys Arg Leu Arg Ser Gln Leu
1 5 10 15
Val Pro Val Arg Ala Leu Gly Leu Gly His Arg Ser Asp Glu Leu Val
20 25 30
Arg Phe Arg Phe Cys Ser Gly Ser Cys Arg Arg Ala Arg Ser Pro His
35 40 45
Asp Leu Ser Leu Ala Ser Leu Leu Gly Ala Gly Ala Leu Arg Pro Pro
50 55 60
Pro Gly Ser Arg Pro Val Ser Gln Pro Cys Cys Arg Pro Thr Arg Tyr
65 70 75 80
Glu Ala Val Ser Phe Met Asp Val Asn Ser Thr Trp Arg Thr Val Asp
85 90 95
Arg Leu Ser Ala Thr Ala Cys Gly Cys Leu Gly
100 105

<210> 41
<211> 106
<212> PRT
<213> Homo sapiens

<400> 41

Ala Arg Ala Ala Gly Ala Arg Gly Cys Arg Leu Arg Ser Gln Leu Val
1 5 10 15
Pro Val Arg Ala Leu Gly Leu Gly His Arg Ser Asp Glu Leu Val Arg
20 25 30
Phe Arg Phe Cys Ser Gly Ser Cys Arg Arg Ala Arg Ser Pro His Asp
35 40 45
Leu Ser Leu Ala Ser Leu Leu Gly Ala Gly Ala Leu Arg Pro Pro Pro
50 55 60
Gly Ser Arg Pro Val Ser Gln Pro Cys Cys Arg Pro Thr Arg Tyr Glu
65 70 75 80
Ala Val Ser Phe Met Asp Val Asn Ser Thr Trp Arg Thr Val Asp Arg
85 90 95
Leu Ser Ala Thr Ala Cys Gly Cys Leu Gly
100 105

<210> 42

<211> 105

<212> PRT

<213> Homo sapiens

<400> 42

Arg Ala Ala Gly Ala Arg Gly Cys Arg Leu Arg Ser Gln Leu Val Pro
1 5 10 15
Val Arg Ala Leu Gly Leu Gly His Arg Ser Asp Glu Leu Val Arg Phe
20 25 30
Arg Phe Cys Ser Gly Ser Cys Arg Arg Ala Arg Ser Pro His Asp Leu
35 40 45
Ser Leu Ala Ser Leu Leu Gly Ala Gly Ala Leu Arg Pro Pro Pro Gly
50 55 60
Ser Arg Pro Val Ser Gln Pro Cys Cys Arg Pro Thr Arg Tyr Glu Ala
65 70 75 80
Val Ser Phe Met Asp Val Asn Ser Thr Trp Arg Thr Val Asp Arg Leu
85 90 95
Ser Ala Thr Ala Cys Gly Cys Leu Gly
100 105

<210> 43

<211> 104

<212> PRT

<213> Homo sapiens

<400> 43

Ala Ala Gly Ala Arg Gly Cys Arg Leu Arg Ser Gln Leu Val Pro Val
1 5 10 15
Arg Ala Leu Gly Leu Gly His Arg Ser Asp Glu Leu Val Arg Phe Arg
20 25 30

Phe Cys Ser Gly Ser Cys Arg Arg Ala Arg Ser Pro His Asp Leu Ser
 35 40 45
 Leu Ala Ser Leu Leu Gly Ala Gly Ala Leu Arg Pro Pro Pro Gly Ser
 50 55 60
 Arg Pro Val Ser Gln Pro Cys Cys Arg Pro Thr Arg Tyr Glu Ala Val
 65 70 75 80
 Ser Phe Met Asp Val Asn Ser Thr Trp Arg Thr Val Asp Arg Leu Ser
 85 90 95
 Ala Thr Ala Cys Gly Cys Leu Gly
 100

<210> 44
 <211> 103
 <212> PRT
 <213> Homo sapiens

<400> 44
 Ala Gly Ala Arg Gly Cys Arg Leu Arg Ser Gln Leu Val Pro Val Arg
 1 5 10 15
 Ala Leu Gly Leu Gly His Arg Ser Asp Glu Leu Val Arg Phe Arg Phe
 20 25 30
 Cys Ser Gly Ser Cys Arg Arg Ala Arg Ser Pro His Asp Leu Ser Leu
 35 40 45
 Ala Ser Leu Leu Gly Ala Gly Ala Leu Arg Pro Pro Pro Gly Ser Arg
 50 55 60
 Pro Val Ser Gln Pro Cys Cys Arg Pro Thr Arg Tyr Glu Ala Val Ser
 65 70 75 80
 Phe Met Asp Val Asn Ser Thr Trp Arg Thr Val Asp Arg Leu Ser Ala
 85 90 95
 Thr Ala Cys Gly Cys Leu Gly
 100

<210> 45
 <211> 102
 <212> PRT
 <213> Homo sapiens

<400> 45
 Gly Ala Arg Gly Cys Arg Leu Arg Ser Gln Leu Val Pro Val Arg Ala
 1 5 10 15
 Leu Gly Leu Gly His Arg Ser Asp Glu Leu Val Arg Phe Arg Phe Cys
 20 25 30
 Ser Gly Ser Cys Arg Arg Ala Arg Ser Pro His Asp Leu Ser Leu Ala
 35 40 45
 Ser Leu Leu Gly Ala Gly Ala Leu Arg Pro Pro Pro Gly Ser Arg Pro
 50 55 60
 Val Ser Gln Pro Cys Cys Arg Pro Thr Arg Tyr Glu Ala Val Ser Phe
 65 70 75 80

Met Asp Val Asn Ser Thr Trp Arg Thr Val Asp Arg Leu Ser Ala Thr
85 90 95

Ala Cys Gly Cys Leu Gly
100

<210> 46
<211> 101
<212> PRT
<213> Homo sapiens

<400> 46
Ala Arg Gly Cys Arg Leu Arg Ser Gln Leu Val Pro Val Arg Ala Leu
1 5 10 15
Gly Leu Gly His Arg Ser Asp Glu Leu Val Arg Phe Arg Phe Cys Ser
20 25 30
Gly Ser Cys Arg Arg Ala Arg Ser Pro His Asp Leu Ser Leu Ala Ser
35 40 45
Leu Leu Gly Ala Gly Ala Leu Arg Pro Pro Pro Gly Ser Arg Pro Val
50 55 60
Ser Gln Pro Cys Cys Arg Pro Thr Arg Tyr Glu Ala Val Ser Phe Met
65 70 75 80
Asp Val Asn Ser Thr Trp Arg Thr Val Asp Arg Leu Ser Ala Thr Ala
85 90 95
Cys Gly Cys Leu Gly
100

<210> 47
<211> 100
<212> PRT
<213> Homo sapiens

<400> 47
Arg Gly Cys Arg Leu Arg Ser Gln Leu Val Pro Val Arg Ala Leu Gly
1 5 10 15
Leu Gly His Arg Ser Asp Glu Leu Val Arg Phe Arg Phe Cys Ser Gly
20 25 30
Ser Cys Arg Arg Ala Arg Ser Pro His Asp Leu Ser Leu Ala Ser Leu
35 40 45
Leu Gly Ala Gly Ala Leu Arg Pro Pro Pro Gly Ser Arg Pro Val Ser
50 55 60
Gln Pro Cys Cys Arg Pro Thr Arg Tyr Glu Ala Val Ser Phe Met Asp
65 70 75 80
Val Asn Ser Thr Trp Arg Thr Val Asp Arg Leu Ser Ala Thr Ala Cys
85 90 95
Gly Cys Leu Gly
100

<210> 48
<211> 99
<212> PRT
<213> Homo sapiens

<400> 48
Gly Cys Arg Leu Arg Ser Gln Leu Val Pro Val Arg Ala Leu Gly Leu
1 5 10 15
Gly His Arg Ser Asp Glu Leu Val Arg Phe Arg Phe Cys Ser Gly Ser
20 25 30
Cys Arg Arg Ala Arg Ser Pro His Asp Leu Ser Leu Ala Ser Leu Leu
35 40 45
Gly Ala Gly Ala Leu Arg Pro Pro Pro Gly Ser Arg Pro Val Ser Gln
50 55 60
Pro Cys Cys Arg Pro Thr Arg Tyr Glu Ala Val Ser Phe Met Asp Val
65 70 75 80
Asn Ser Thr Trp Arg Thr Val Asp Arg Leu Ser Ala Thr Ala Cys Gly
85 90 95
Cys Leu Gly

<210> 49
<211> 197
<212> PRT
<213> Homo sapiens

<400> 49
Met Gln Arg Trp Lys Ala Ala Ala Leu Ala Ser Val Leu Cys Ser Ser
1 5 10 15
Val Leu Ser Ile Trp Met Cys Arg Glu Gly Leu Leu Leu Ser His Arg
20 25 30
Leu Gly Pro Ala Leu Val Pro Leu His Arg Leu Pro Arg Thr Leu Asp
35 40 45
Ala Arg Ile Ala Arg Leu Ala Gln Tyr Arg Ala Leu Leu Gln Gly Ala
50 55 60
Pro Asp Ala Met Glu Leu Arg Glu Leu Thr Pro Trp Ala Gly Arg Pro
65 70 75 80
Pro Gly Pro Arg Arg Arg Ala Gly Pro Arg Arg Arg Arg Ala Arg Ala
85 90 95
Arg Leu Gly Ala Arg Pro Cys Gly Leu Arg Glu Leu Glu Val Arg Val
100 105 110
Ser Glu Leu Gly Leu Gly Tyr Ala Ser Asp Glu Thr Val Leu Phe Arg
115 120 125
Tyr Cys Ala Gly Ala Cys Glu Ala Ala Ala Arg Val Tyr Asp Leu Gly
130 135 140
Leu Arg Arg Leu Arg Gln Arg Arg Arg Leu Arg Arg Glu Arg Val Arg
145 150 155 160

Ala Gln Pro Cys Cys Arg Pro Thr Ala Tyr Glu Asp Glu Val Ser Phe
165 170 175
Leu Asp Ala His Ser Arg Tyr His Thr Val His Glu Leu Ser Ala Arg
180 185 190
Glu Cys Ala Cys Val
195

<210> 50
<211> 156
<212> PRT
<213> Homo sapiens

<400> 50
Met Ala Val Gly Lys Phe Leu Leu Gly Ser Leu Leu Leu Leu Ser Leu
1 5 10 15
Gln Leu Gly Gln Gly Trp Gly Pro Asp Ala Arg Gly Val Pro Val Ala
20 25 30
Asp Gly Glu Phe Ser Ser Glu Gln Val Ala Lys Ala Gly Gly Thr Trp
35 40 45
Leu Gly Thr His Arg Pro Leu Ala Arg Leu Arg Arg Ala Leu Ser Gly
50 55 60
Pro Cys Gln Leu Trp Ser Leu Thr Leu Ser Val Ala Glu Leu Gly Leu
65 70 75 80
Gly Tyr Ala Ser Glu Lys Val Ile Phe Arg Tyr Cys Ala Gly Ser
85 90 95
Cys Pro Arg Gly Ala Arg Thr Gln His Gly Leu Ala Leu Ala Arg Leu
100 105 110
Gln Gly Gln Gly Arg Ala His Gly Gly Pro Cys Cys Arg Pro Thr Arg
115 120 125
Tyr Thr Asp Val Ala Phe Leu Asp Asp Arg His Arg Trp Gln Arg Leu
130 135 140
Pro Gln Leu Ser Ala Ala Ala Cys Gly Cys Gly Gly
145 150 155

<210> 51
<211> 211
<212> PRT
<213> Homo sapiens

<400> 51
Met Lys Leu Trp Asp Val Val Ala Val Cys Leu Val Leu Leu His Thr
1 5 10 15
Ala Ser Ala Phe Pro Leu Pro Ala Gly Lys Arg Pro Pro Glu Ala Pro
20 25 30
Ala Glu Asp Arg Ser Leu Gly Arg Arg Arg Ala Pro Phe Ala Leu Ser
35 40 45
Ser Asp Ser Asn Met Pro Glu Asp Tyr Pro Asp Gln Phe Asp Asp Val
50 55 60

Met Asp Phe Ile Gln Ala Thr Ile Lys Arg Leu Lys Arg Ser Pro Asp
 65 70 75 80
 Lys Gln Met Ala Val Leu Pro Arg Arg Glu Arg Asn Arg Gln Ala Ala
 85 90 95
 Ala Ala Asn Pro Glu Asn Ser Arg Gly Lys Gly Arg Arg Gly Gln Arg
 100 105 110
 Gly Lys Asn Arg Gly Cys Val Leu Thr Ala Ile His Leu Asn Val Thr
 115 120 125
 Asp Leu Gly Leu Gly Tyr Glu Thr Lys Glu Glu Leu Ile Phe Arg Tyr
 130 135 140
 Cys Ser Gly Ser Cys Asp Ala Ala Glu Thr Thr Tyr Asp Lys Ile Leu
 145 150 155 160
 Lys Asn Leu Ser Arg Asn Arg Arg Leu Val Ser Asp Lys Val Gly Gln
 165 170 175
 Ala Cys Cys Arg Pro Ile Ala Phe Asp Asp Asp Leu Ser Phe Leu Asp
 180 185 190
 Asp Asn Leu Val Tyr His Ile Leu Arg Lys His Ser Ala Lys Arg Cys
 195 200 205
 Gly Cys Ile
 210

<210> 52
 <211> 365
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:synthetic gene
 for Neublastin

<400> 52
 taccatggct ggaggaccgg gatctcgtgc tcgtgcagca ggagcacgtg gctgtcgtct 60
 gcgttctcaa ctagtgccgg tgcgtgcact cggactggga caccgttccg acgaactagt 120
 acgttttcgt ttttgttcag gatcttgtcg tcgtgcacgt tctccgcatg atctatctct 180
 agcatctcta ctaggagccg gagcactaag accgccgccg ggatctagac ctgtatctca 240
 acctgttgt agacctacta gatacgaagc agtatctttc atggacgtaa actctacatg 300
 gagaaccgta gatagactat ctgcaaccgc atgtggctgt ctaggatgat aatagggatc 360
 cggct 365

<210> 53
 <211> 365
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:synthetic gene
 for Neublastin

<400> 53
 atggtaccga cctcctggcc ctagagcacg agcacgtcgt cctcgtgcac cgacagcaga 60
 cgcaagagtt gatcacggcc acgcacgtga gcctgacct gtggcaaggc tgcttgatca 120
 tgcaaaagca aaaacaagtc ctagaacagc agcacgtgca agaggcgtac tagatagaga 180

```

tcgtagagat gatcctcggc ctcgtgattc tggcggcggc cctagatctg gacatagagt 240
tggaacaaca tctggatgat ctatgcttcg tcatagaaag tacctgcatt tgagatgtac 300
ctcttggcat ctatctgata gacgttggcg tacaccgaca gatcctacta ttatccctag 360
gccga 365

```

<210> 54
 <211> 114
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:synthetic
 Neublabin

<400> 54
 Met Ala Gly Gly Pro Gly Ser Arg Ala Arg Ala Ala Gly Ala Arg Gly
 1 5 10 15
 Cys Arg Leu Arg Ser Gln Leu Val Pro Val Arg Ala Leu Gly Leu Gly
 20 25 30
 His Arg Ser Asp Glu Leu Val Arg Phe Arg Phe Cys Ser Gly Ser Cys
 35 40 45
 Arg Arg Ala Arg Ser Pro His Asp Leu Ser Leu Ala Ser Leu Leu Gly
 50 55 60
 Ala Gly Ala Leu Arg Pro Pro Pro Gly Ser Arg Pro Val Ser Gln Pro
 65 70 75 80
 Cys Cys Arg Pro Thr Arg Tyr Glu Ala Val Ser Phe Met Asp Val Asn
 85 90 95
 Ser Thr Trp Arg Thr Val Asp Arg Leu Ser Ala Thr Ala Cys Gly Cys
 100 105 110
 Leu Gly

<210> 55
 <211> 442
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:synthetic gene
 for HisNeublabin

<400> 55
 taccatgggc catcatcatc atcatcatca tcatcatcac tcgagcggcc atatcgacga 60
 cgacgacaag gctggaggac cgggatctcg tgctcgtgca gcaggagcac gtggctgtcg 120
 tctgcgttct caactagtgc cgggtgcgtgc actcggactg ggacaccggt ccgacgaact 180
 agtacgtttt cgtttttgtt caggatcttg tcgtcgtgca cgttctccgc atgatctatc 240
 tctagcatct ctactaggag cgggagcact aagaccgccc ccgggatcta gacctgtatc 300
 tcaaccttgt tgtagaccta ctagatacga agcagtatct ttcatggacg taaactctac 360
 atggagaacc gtagatagac tatctgcaac cgcattgtggc tgtctaggat gataataggg 420
 atccggctgc taacaaagcc cg 442

<210> 56
 <211> 442
 <212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:synthetic gene
for HisNeublastin

<400> 56

```
atggtacccg gtagtagtag tagtagtagt agtagtagtg agctcgccgg tatagctgct 60
gctgctgttc cgacctcctg gccctagagc acgagcacgt cgtcctcgtg caccgacagc 120
agacgcaaga gttgatcacg gccacgcacg tgagcctgac cctgtggcaa ggctgcttga 180
tcatgcaaaa gcaaaaacaa gtcctagaac agcagcacgt gcaagaggcg tactagatag 240
agatcgtaga gatgatcctc ggctcgtga ttctggcggc ggccctagat ctggacatag 300
agttggaaca acatctggat gatctatgct tcgtcataga aagtacctgc atttgagatg 360
tacctcttgg catctatctg atagacgttg gcgtacaccg acagatccta ctattatccc 420
taggcgcagc attgtttcgg gc                                         442
```

<210> 57

<211> 135

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:synthetic
HisNeublastin

<400> 57

```
Met Gly His His His His His His His His His Ser Ser Gly His
 1                               5                               10          15

Ile Asp Asp Asp Asp Lys Ala Gly Gly Pro Gly Ser Arg Ala Arg Ala
      20                      25                      30

Ala Gly Ala Arg Gly Cys Arg Leu Arg Ser Gln Leu Val Pro Val Arg
      35                      40                      45

Ala Leu Gly Leu Gly His Arg Ser Asp Glu Leu Val Arg Phe Arg Phe
      50                      55                      60

Cys Ser Gly Ser Cys Arg Arg Ala Arg Ser Pro His Asp Leu Ser Leu
      65                      70                      75                      80

Ala Ser Leu Leu Gly Ala Gly Ala Leu Arg Pro Pro Pro Gly Ser Arg
      85                      90                      95

Pro Val Ser Gln Pro Cys Cys Arg Pro Thr Arg Tyr Glu Ala Val Ser
      100                     105                     110

Phe Met Asp Val Asn Ser Thr Trp Arg Thr Val Asp Arg Leu Ser Ala
      115                     120                     125

Thr Ala Cys Gly Cys Leu Gly
      130                     135
```